

SEQUENCE LISTING

<110> Gentz et al.

<120> Therapeutic Compositions and Methods for Treating Disease States with Myeloid Progenitor Inhibitory Factor-1 (MPIF-1), Monocyte Colony Inhibitory Factor (M-CIF), and Macrophage Inhibitory Factor-4 (MIP-4)

<130> PF111U3C1D1

<150> US 09/571,013
<151> 2000-05-15

<150> US 08/941,020
<151> 1997-09-30

<150> US 60/027,299
<151> 1996-09-30

<150> US 08/722,719
<151> 1996-09-30

<150> US 08/722,723
<151> 1996-09-30

<150> US 60/027,300
<151> 1996-09-30

<150> US 08/468,775
<151> 1995-06-06

<150> US 08/465,682
<151> 1995-06-06

<150> US 08/446,881
<151> 1995-05-05

<150> US 08/173,209
<151> 1993-12-22

<150> US 08/208,339
<151> 1994-03-08

<160> 60

<170> PatentIn version 3.2

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Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile		
1				5					10					15			
gcc	cta	ggg	acc	aag	act	gaa	tcc	tcc	tca	cgg	gga	cct	tac	cac	ccc		96
Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro		
			20					25					30				
tca	gag	tgc	tgc	ttc	acc	tac	act	acc	tac	aag	atc	ccg	cgt	cag	cgg		144
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg		
		35					40					45					
att	atg	gat	tac	tat	gag	acc	aac	agc	cag	tgc	tcc	aag	ccc	gga	att		192
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile		
	50					55					60						
gtc	ttc	atc	acc	aaa	agg	ggc	cat	tcc	gtc	tgt	acc	aac	ccc	agt	gac		240
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp		
65					70					75					80		
aag	tgg	gtc	cag	gac	tat	atc	aag	gac	atg	aag	gag	aac	tga				282
Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn					
				85					90								

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Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro		
			20					25					30				
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg		
		35					40					45					
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile		
	50					55					60						
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp		
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Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn					
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 ctt gga tcc cag gcc cgg gtc aca aaa gat gca gag aca gag ttc atg 96
 Leu Gly Ser Gln Ala Arg Val Thr Lys Asp Ala Glu Thr Glu Phe Met
 20 25 30
 atg tca aag ctt cca ttg gaa aat cca gta ctt ctg gac aga ttc cat 144
 Met Ser Lys Leu Pro Leu Glu Asn Pro Val Leu Leu Asp Arg Phe His
 35 40 45
 gct act agt gct gac tgc tgc atc tcc tac acc cca cga agc atc ccg 192
 Ala Thr Ser Ala Asp Cys Cys Ile Ser Tyr Thr Pro Arg Ser Ile Pro
 50 55 60
 tgt tca ctc ctg gag agt tac ttt gaa acg aac agc gag tgc tcc aag 240
 Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys
 65 70 75 80
 ccg ggt gtc atc ttc ctc acc aag aag ggg cga cgt ttc tgt gcc aac 288
 Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn
 85 90 95
 ccc agt gat aag caa gtt cag gtt tgc atg aga atg ctg aag ctg gac 336
 Pro Ser Asp Lys Gln Val Gln Val Cys Met Arg Met Leu Lys Leu Asp
 100 105 110
 aca cgg atc aag acc agg aag aat tga 363
 Thr Arg Ile Lys Thr Arg Lys Asn
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 20 25 30
 Met Ser Lys Leu Pro Leu Glu Asn Pro Val Leu Leu Asp Arg Phe His
 35 40 45
 Ala Thr Ser Ala Asp Cys Cys Ile Ser Tyr Thr Pro Arg Ser Ile Pro
 50 55 60

Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys
65 70 75 80

Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn
85 90 95

Pro Ser Asp Lys Gln Val Gln Val Cys Met Arg Met Leu Lys Leu Asp
100 105 110

Thr Arg Ile Lys Thr Arg Lys Asn
115 120

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ctc tgc tcc tgt gca caa gtt ggt acc aac aaa gag ctc tgc tgc ctc 96
Leu Cys Ser Cys Ala Gln Val Gly Thr Asn Lys Glu Leu Cys Cys Leu
20 25 30
gtc tat acc tcc tgg cag att cca caa aag ttc ata gtt gac tat tct 144
Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
35 40 45
gaa acc agc ccc cag tgc ccc aag cca ggt gtc atc ctc cta acc aag 192
Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
50 55 60
aga ggc cgg cag atc tgt gct gac ccc aat aag aag tgg gtc cag aaa 240
Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65 70 75 80
tac atc agc gac ctg aag ctg aat gcc tga 270
Tyr Ile Ser Asp Leu Lys Leu Asn Ala
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<213> Homo sapiens

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Met Lys Gly Leu Ala Ala Ala Leu Leu Val Leu Val Cys Thr Met Ala
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Leu Cys Ser Cys Ala Gln Val Gly Thr Asn Lys Glu Leu Cys Cys Leu
 20 25 30

Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
 35 40 45

Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
 50 55 60

Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
 65 70 75 80

Tyr Ile Ser Asp Leu Lys Leu Asn Ala
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<210> 7
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Met Arg Val Thr Lys Asp Ala Glu Thr Glu Phe Met Met Ser Lys Leu
 1 5 10 15

Pro Leu Glu Asn Pro Val Leu Leu Asp Arg Phe His Ala Thr Ser Ala
 20 25 30

Asp Cys Cys Ile Ser Tyr Thr Pro Arg Ser Ile Pro Cys Ser Leu Leu
 35 40 45

Glu Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys Pro Gly Val Ile
 50 55 60

Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys
 65 70 75 80

Gln Val Gln Val Cys Met Arg Met Leu Lys Leu Asp Thr Arg Ile Lys
 85 90 95

Thr Arg Lys Asn
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<400> 8

Met Arg Phe His Ala Thr Ser Ala Asp Cys Cys Ile Ser Tyr Thr Pro
 1 5 10 15

Arg Ser Ile Pro Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr Asn Ser
 20 25 30

Glu Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg Arg
 35 40 45

Phe Cys Ala Asn Pro Ser Asp Lys Gln Val Gln Val Cys Met Arg Met
 50 55 60

Leu Lys Leu Asp Thr Arg Ile Lys Thr Arg Lys Asn
 65 70 75

<210> 9
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His Ala Ala Gly Phe His Ala Thr Ser Ala Asp Cys Cys Ile Ser Tyr
 1 5 10 15

Thr Pro Arg Ser Ile Pro Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr
 20 25 30

Asn Ser Glu Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Lys Gly
 35 40 45

Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys Gln Val Gln Val Cys Met
 50 55 60

Arg Met Leu Lys Leu Asp Thr Arg Ile Lys Thr Arg Lys Asn
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Leu Ser Cys Leu Met Leu Val Thr Ala Leu Gly Ser Gln Ala Arg Val
10 15 20

aca aaa gat gca gag aca gag ttg acg atg tca aag ctt cca ttg gaa 151
Thr Lys Asp Ala Glu Thr Glu Leu Thr Met Ser Lys Leu Pro Leu Glu
25 30 35

aat cca gta ctt ctg gac atg ctc tgg agg aga aag att ggt cct cag 199
Asn Pro Val Leu Leu Asp Met Leu Trp Arg Arg Lys Ile Gly Pro Gln
40 45 50 55

atg acc ctt tct cat gcc gca gga ttc cat gct act agt gct gac tgc 247
Met Thr Leu Ser His Ala Ala Gly Phe His Ala Thr Ser Ala Asp Cys
60 65 70

tgc atg tcc tac acc cca cga agc atc ccg tgt tca ctc ctg gag agt 295
Cys Met Ser Tyr Thr Pro Arg Ser Ile Pro Cys Ser Leu Leu Glu Ser
75 80 85

tac ttt gaa acg aac agc gag tgc tcc aag ccg ggt gtc atc ttc ctc 343
Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys Pro Gly Val Ile Phe Leu
90 95 100

acc aag aag ggg cga cgt ttc tgt gcc aac ccc agt gat aag caa gtt 391
Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys Gln Val
105 110 115

cag gtt tgc atg aga atg ctg aag ctg gac aca cgg atc aag acc agg 439
Gln Val Cys Met Arg Met Leu Lys Leu Asp Thr Arg Ile Lys Thr Arg
120 125 130 135

aag aat tga acttgtcaag gtgaagggga cacaagttgc cagccaccaa 488
Lys Asn

ctttcttgcc tcaactaact tctgaattc tttttttaag aagcatttat tcttgtgttc 548

tggtattaga gcaattcatc ttttctcacc tttaaaaaaa aaaaaaaaaa a 599

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<213> Homo sapiens

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 20 25 30

Met Ser Lys Leu Pro Leu Glu Asn Pro Val Leu Leu Asp Met Leu Trp
 35 40 45

Arg Arg Lys Ile Gly Pro Gln Met Thr Leu Ser His Ala Ala Gly Phe
 50 55 60

His Ala Thr Ser Ala Asp Cys Cys Met Ser Tyr Thr Pro Arg Ser Ile
 65 70 75 80

Pro Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser
 85 90 95

Lys Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala
 100 105 110

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 115 120 125

Asp Thr Arg Ile Lys Thr Arg Lys Asn
 130 135

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26

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 cgctctagag taaaacgacg gccagt

26

<210> 14
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 <400> 14
 cccgcatgcg ggtcacaaaa gatgcag 27

<210> 15
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 <212> DNA
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 <223> Primer
 <400> 15
 aaaggatcct caattcttcc tggcttt 27

<210> 16
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 <212> DNA
 <213> Artificial sequence
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 <223> Primer
 <400> 16
 acatgcatgc guguuaccaa agacgcugaa accgaauuca ugaugucc 48

<210> 17
 <211> 36
 <212> DNA
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 <223> Primer
 <400> 17
 gccgaagctt tcagttttta cgggttttga tacggg 36

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 acccgguucu gcuggaccgu uuccacgc 88

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 caaaaaaggu cgucguuucu ggcuaaccc guccgacaaa cagg 104

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 ctgaacctgt ttgtcggacg gcttagcgc 89

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 gcagtcagcg gaggtagcgt ggaaacggtc cagc 94

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 <223> Primer

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 <211> 83
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Cys Cys Ile Ser Tyr Thr Pro Arg Ser Ile Pro Cys Ser Leu Leu Glu
 20 25 30

Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys Pro Gly Val Ile Phe
 35 40 45

Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys Gln
 50 55 60

Val Gln Val Cys Met Arg Met Leu Lys Leu Asp Thr Arg Ile Lys Thr
 65 70 75 80

Arg Lys Asn

<210> 24
 <211> 35
 <212> DNA
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<220>
 <223> Primer

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 <211> 84
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<400> 25

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Asp Cys Cys Ile Ser Tyr Thr Pro Arg Ser Ile Pro Cys Ser Leu Leu
 20 25 30

Glu Ser Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys Pro Gly Val Ile
 35 40 45

Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys
 50 55 60

Gln Val Gln Val Cys Met Arg Met Leu Lys Leu Asp Thr Arg Ile Lys

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70

75

80

Thr Arg Lys Asn

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32

<210> 27

<211> 77

<212> PRT

<213> Homo sapiens

<400> 27

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 1 5 10 15

Pro Arg Ser Ile Pro Cys Ser Leu Leu Glu Ser Tyr Phe Glu Thr Asn
 20 25 30

Ser Glu Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg
 35 40 45

Arg Phe Cys Ala Asn Pro Ser Asp Lys Gln Val Gln Val Cys Met Arg
 50 55 60

Met Leu Lys Leu Asp Thr Arg Ile Lys Thr Arg Lys Asn
 65 70 75

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<211> 29

<212> DNA

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20 25 30

Lys Pro Gly Val Ile Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala
35 40 45

Asn Pro Ser Asp Lys Gln Val Gln Val Cys Met Arg Met Leu Lys Leu
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Asp Thr Arg Ile Lys Thr Arg Lys Asn
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21

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 20 25 30

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 35 40 45

Glu Ala Tyr Phe Glu Thr Asn Ser Glu Cys Ser Lys Pro Gly Val Ile
 50 55 60

Phe Leu Thr Lys Lys Gly Arg Arg Phe Cys Ala Asn Pro Ser Asp Lys
 65 70 75 80

Gln Val Gln Val Cys Met Arg Met Leu Lys Leu Asp Thr Arg Ile Lys
 85 90 95

Thr Arg Lys Asn
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 aaaaagcttt cagttctcct tcatgtc 27

 <210> 43
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 <220>
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<210> 46
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 <400> 46
 aaaggatcct caattcttcc aggtctt 27

 <210> 47
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 <212> DNA
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 <220>
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 <400> 47
 ggaaagctta tgaagggcct tgcagctgcc 30

 <210> 48
 <211> 57
 <212> DNA
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 <220>
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 <211> 33
 <212> DNA
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 <220>
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 <210> 50
 <211> 27
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 aaaggatcct caggcattca gcttcag 27

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 ggaaagctta tgaagattcc gtggctgc 28

 <210> 52
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 <212> DNA
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 <210> 53
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 aaaggatccg ccaccatgaa gatctccgtg gct 33

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 <211> 92
 <212> PRT
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20

25

30

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
 35 40 45

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
 50 55 60

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
 65 70 75 80

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
 85 90

<210> 56
 <211> 4208
 <212> DNA
 <213> Homo sapiens

<400> 56
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 ccacgctacc tccgctgact gctgcatctc ctacaccccg cgttccatcc cgtgctcgct 180
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 caaaaaaggt cgtcgtttct gcgctaaccg gtccgacaaa caggttcagg tttgtatgcg 300
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Ile	Phe	Leu	Thr	Lys	Lys	Gly	Arg	Arg	Phe	Cys	Ala	Asn	Pro	Ser	Asp
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Lys	Thr	Arg	Lys	Asn
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